

## SEQUENCE LISTING

10/593842

<110> Nakamura, Yusuke  
Daigo, Yataro  
Nakatsuru, Shuichi

<120> METHOD FOR DIAGNOSING NON-SMALL CELL  
LUNG CANCER

<130> 082368-000510US

<150> PCT/JP2005/005613

<151> 2005-03-18

<150> US 60/555,789

<151> 2004-03-23

<160> 127

<170> PatentIn version 3.3

<210> 1

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Ala Leu Asp Thr Ile Thr Thr Val Ala Leu Gly Ser Leu Thr Ser Ile  
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Pro Glu Asn Val Ser Thr His Val Ser Gln Ile Phe Asn Met Ile Leu  
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Lys Glu Gln Ser Leu Ala Ala Glu Ser Lys Thr Val Leu Gln Glu Leu  
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Ile Asn Val Leu Lys Thr Asp Leu Leu Ser Ser Leu Glu Met Ile Leu  
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Ser Pro Thr Val Val Ser Ile Leu Lys Ile Asn Ser Gln Leu Lys His  
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Ile Phe Lys Thr Ser Leu Thr Val Ala Asp Lys Ile Glu Asp Gln Lys  
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Lys Glu Leu Asp Gly Phe Leu Ser Ile Leu Cys Asn Asn Leu His Glu  
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Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile Lys Gln Thr His Ser Gln  
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Glu Leu Cys Lys Leu Met Asn Leu Trp Thr Glu Arg Phe Cys Ala Leu  
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Glu Glu Lys Cys Glu Asn Ile Gln Lys Pro Leu Ser Ser Val Gln Glu  
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Asn Ile Gln Gln Lys Ser Lys Asp Ile Val Asn Lys Met Thr Phe His  
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Ser Gln Lys Phe Cys Ala Asp Ser Asp Gly Phe Ser Gln Glu Leu Arg  
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Asn Phe Asn Gln Glu Gly Thr Lys Leu Val Glu Glu Ser Val Lys His  
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Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys Ile Ser Gln Glu Thr Glu  
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Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr Val Tyr Phe Ser Glu Gln  
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Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu Leu His Asn Leu Leu  
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Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser Ser Asp Ile Thr Glu  
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Lys Ser Asp Gly Arg Lys Ala Ala His Glu Lys Gln His Asn Ile Phe  
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Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr Lys Leu Asn Cys Phe  
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Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr Gly Thr Thr Pro Gln  
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Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu Thr Ile Pro Asp Val  
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Gln Glu Pro Ser Val Asp Ala Gly Val Asp Cys Ser Ser Ile Gly Gly  
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 Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met  
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Leu																		

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Thr Cys Val Ala Leu Phe Val Val Gly Ile Ala Gly Asn Leu Leu Thr  
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Met Leu Val Val Ser Arg Phe Arg Glu Leu Arg Thr Thr Thr Asn Leu  
 65 70 75 80

Tyr Leu Ser Ser Met Ala Phe Ser Asp Leu Leu Ile Phe Leu Cys Met  
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Pro Leu Asp Leu Val Arg Leu Trp Gln Tyr Arg Pro Trp Asn Phe Gly  
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Asp Leu Leu Cys Lys Leu Phe Gln Phe Val Ser Glu Ser Cys Thr Tyr  
 115 120 125

Ala Thr Val Leu Thr Ile Thr Ala Leu Ser Val Glu Arg Tyr Phe Ala  
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Lys Leu Val Ile Phe Val Ile Trp Ala Val Ala Phe Cys Ser Ala Gly  
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Pro Ile Phe Val Leu Val Gly Val Glu His Glu Asn Gly Thr Asp Pro  
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Trp Asp Thr Asn Glu Cys Arg Pro Thr Glu Phe Ala Val Arg Ser Gly  
 195 200 205

Leu Leu Thr Val Met Val Trp Val Ser Ser Ile Phe Phe Phe Leu Pro  
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Val Phe Cys Leu Thr Val Leu Tyr Ser Leu Ile Gly Arg Lys Leu Trp  
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Arg Arg Arg Arg Gly Asp Ala Val Val Gly Ala Ser Leu Arg Asp Gln  
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Asn His Lys Gln Thr Val Lys Met Leu Gly Gly Ser Gln Arg Ala Leu  
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 ctg ctg gcc ccg ggc ttc ggc aac gct tcg ggc aac gcg tcg gag cgc 507  
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Val Arg Arg Leu Met Phe Cys Tyr Ile Ser Asp Glu Gln Trp Thr Pro  
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Phe Tyr Val Ser Ser Thr Ile Asn Pro Ile Leu Tyr Asn Leu Val Ser  
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Ala Asn Phe Arg His Ile Phe Leu Ala Thr Leu Ala Cys Leu Cys Pro  
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Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser  
 35 40 45

Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His  
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Gly Lys Pro Ile Glu Val Glu His Ser Val Pro Lys Arg Gln Arg Ile  
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Arg Lys Leu Gln Ile Arg Asn Ile Pro Pro His Leu Gln Trp Glu Val  
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Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln  
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Phe Leu Val Lys Thr Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu Ser
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Trp Ala Leu Lys Ala Ile Glu Ala Leu Ser Gly Lys Ile Glu Leu His
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130 135 140

Glu Asn Phe Thr Leu Lys Val Ala Tyr Ile Pro Asp Glu Met Ala Ala  
145 150 155 160

Gln Gln Asn Pro Leu Gln Gln Pro Arg Gly Arg Arg Gly Leu Gly Gln  
165 170 175

Arg Gly Ser Ser Arg Gln Gly Ser Pro Gly Ser Val Ser Lys Gln Lys  
180 185 190

Pro Cys Asp Leu Pro Leu Arg Leu Leu Val Pro Thr Gln Phe Val Gly  
195 200 205

Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln  
210 215 220

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Cys Lys Ser Ile Leu Glu Ile Met His Lys Glu Ala Gln Asp Ile Lys  
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Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Asn Val Glu Thr Cys  
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Ala Lys Val Arg Met Val Ile Ile Thr Gly Pro Pro Glu Ala Gln Phe				
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Ser Pro Lys Glu Glu Val Lys Leu Glu Ala His Ile Arg Val Pro Ser				
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Phe Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu				
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Leu Gln Asn Leu Ser Ser Ala Glu Val Val Val Pro Arg Asp Gln Thr				
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Pro Asp Glu Asn Asp Gln Val Val Val Lys Ile Thr Gly His Phe Tyr				
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Ala Cys Gln Val Ala Gln Arg Lys Ile Gln Glu Ile Leu Thr Gln Val				
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agctacggcc taacggcggc ggcgactgca gtctggaggg tccacacttg tgattctcaa      240

tggagagtga aaacgcagat tcata atg aaa act agc ccc cgt cgg cca ctg      292
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att ctc aaa aga cgg agg ctg ccc ctt cct gtt caa aat gcc cca agt      340
Ile Leu Lys Arg Arg Arg Leu Pro Leu Pro Val Gln Asn Ala Pro Ser
10                               15                               20                               25

gaa aca tca gag gag gaa cct aag aga tcc cct gcc caa cag gag tct      388
Glu Thr Ser Glu Glu Glu Pro Lys Arg Ser Pro Ala Gln Gln Glu Ser
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aat caa gca gag gcc tcc aag gaa gtg gca gag tcc aac tct tgc aag      436
Asn Gln Ala Glu Ala Ser Lys Glu Val Ala Glu Ser Asn Ser Cys Lys
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caa gta gtg gcc atc ccc aac aat gct aat att cac agc atc atc aca      532
Gln Val Val Ala Ile Pro Asn Asn Ala Asn Ile His Ser Ile Ile Thr
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gca ctg act gcc aag gga aaa gag agt ggc agt agt ggg ccc aac aaa      580
Ala Leu Thr Ala Lys Gly Lys Glu Ser Gly Ser Ser Gly Pro Asn Lys
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cgg cct caa acc caa acc agc tat gat gcc aaa agg aca gaa gtg acc      676
Arg Pro Gln Thr Gln Thr Ser Tyr Asp Ala Lys Arg Thr Glu Val Thr
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ctg gag acc ttg gga cca aaa cct gca gct agg gat gtg aat ctt cct      724
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140                               145                               150

aga cca cct gga gcc ctt tgc gag cag aaa cgg gag acc tgt gca gat      772
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Asn Ser Thr Glu Arg Lys Arg Met Thr Leu Lys Asp Ile Tyr Thr Trp	
250 255 260 265	
att gag gac cac ttt ccc tac ttt aag cac att gcc aag cca ggc tgg	1108
Ile Glu Asp His Phe Pro Tyr Phe Lys His Ile Ala Lys Pro Gly Trp	
270 275 280	
aag aac tcc atc cgc cac aac ctt tcc ctg cac gac atg ttt gtc cgg	1156
Lys Asn Ser Ile Arg His Asn Leu Ser Leu His Asp Met Phe Val Arg	
285 290 295	
gag acg tct gcc aat ggc aag gtc tcc ttc tgg acc att cac ccc agt	1204
Glu Thr Ser Ala Asn Gly Lys Val Ser Phe Trp Thr Ile His Pro Ser	
300 305 310	
gcc aac cgc tac ttg aca ttg gac cag gtg ttt aag cag cag aaa cga	1252
Ala Asn Arg Tyr Leu Thr Leu Asp Gln Val Phe Lys Gln Gln Lys Arg	
315 320 325	
ccg aat cca gag ctc cgc cgg aac atg acc atc aaa acc gaa ctc ccc	1300
Pro Asn Pro Glu Leu Arg Arg Asn Met Thr Ile Lys Thr Glu Leu Pro	
330 335 340 345	
ctg ggc gca cgg cgg aag atg aag cca ctg cta cca cgg gtc agc tca	1348
Leu Gly Ala Arg Arg Lys Met Lys Pro Leu Leu Pro Arg Val Ser Ser	
350 355 360	
tac ctg gta cct atc cag ttc ccg gtg aac cag tca ctg gtg ttg cag	1396
Tyr Leu Val Pro Ile Gln Phe Pro Val Asn Gln Ser Leu Val Leu Gln	
365 370 375	
ccc tcg gtg aag gtg cca ttg ccc ctg gcg gct tcc ctc atg agc tca	1444
Pro Ser Val Lys Val Pro Leu Pro Leu Ala Ala Ser Leu Met Ser Ser	
380 385 390	
gag ctt gcc cgc cat agc aag cga gtc cgc att gcc ccc aag gtg ctg	1492
Glu Leu Ala Arg His Ser Lys Arg Val Arg Ile Ala Pro Lys Val Leu	
395 400 405	

cta gct gag gag ggg ata gct cct ctt tct tct gca gga cca ggg aaa	1540
Leu Ala Glu Glu Gly Ile Ala Pro Leu Ser Ser Ala Gly Pro Gly Lys	
410 415 420 425	
gag gag aaa ctc ctg ttt gga gaa ggg ttt tct cct ttg ctt cca gtt	1588
Glu Glu Lys Leu Leu Phe Gly Glu Gly Phe Ser Pro Leu Leu Pro Val	
430 435 440	
cag act atc aag gag gaa gaa atc cag cct ggg gag gaa atg cca cac	1636
Gln Thr Ile Lys Glu Glu Glu Ile Gln Pro Gly Glu Glu Met Pro His	
445 450 455	
tta gcg aga ccc atc aaa gtg gag agc cct ccc ttg gaa gag tgg ccc	1684
Leu Ala Arg Pro Ile Lys Val Glu Ser Pro Pro Leu Glu Glu Trp Pro	
460 465 470	
tcc ccg gcc cca tct ttc aaa gag gaa tca tct cac tcc tgg gag gat	1732
Ser Pro Ala Pro Ser Phe Lys Glu Glu Ser Ser His Ser Trp Glu Asp	
475 480 485	
tcg tcc caa tct ccc acc cca aga ccc aag aag tcc tac agt ggg ctt	1780
Ser Ser Gln Ser Pro Thr Pro Arg Pro Lys Lys Ser Tyr Ser Gly Leu	
490 495 500 505	
agg tcc cca acc cgg tgt gtc tcg gaa atg ctt gtg att caa cac agg	1828
Arg Ser Pro Thr Arg Cys Val Ser Glu Met Leu Val Ile Gln His Arg	
510 515 520	
gag agg agg gag agg agc cgg tct cgg agg aaa cag cat cta ctg cct	1876
Glu Arg Arg Glu Arg Ser Arg Ser Arg Arg Lys Gln His Leu Leu Pro	
525 530 535	
ccc tgt gtg gat gag ccg gag ctg ctc ttc tca gag ggg ccc agt act	1924
Pro Cys Val Asp Glu Pro Glu Leu Leu Phe Ser Glu Gly Pro Ser Thr	
540 545 550	
tcc cgc tgg gcc gca gag ctc ccg ttc cca gca gac tcc tct gac cct	1972
Ser Arg Trp Ala Ala Glu Leu Pro Phe Pro Ala Asp Ser Ser Asp Pro	
555 560 565	
gcc tcc cag ctc agc tac tcc cag gaa gtg gga gga cct ttt aag aca	2020
Ala Ser Gln Leu Ser Tyr Ser Gln Glu Val Gly Gly Pro Phe Lys Thr	
570 575 580 585	
ccc att aag gaa acg ctg ccc atc tcc tcc acc ccg agc aaa tct gtc	2068
Pro Ile Lys Glu Thr Leu Pro Ile Ser Ser Thr Pro Ser Lys Ser Val	
590 595 600	
ctc ccc aga acc cct gaa tcc tgg agg ctc acg ccc cca gcc aaa gta	2116
Leu Pro Arg Thr Pro Glu Ser Trp Arg Leu Thr Pro Pro Ala Lys Val	
605 610 615	
ggg gga ctg gat ttc agc cca gta caa acc tcc cag ggt gcc tct gac	2164
Gly Gly Leu Asp Phe Ser Pro Val Gln Thr Ser Gln Gly Ala Ser Asp	
620 625 630	
ccc ttg cct gac ccc ctg ggg ctg atg gat ctc agc acc act ccc ttg	2212
Pro Leu Pro Asp Pro Leu Gly Leu Met Asp Leu Ser Thr Thr Pro Leu	
635 640 645	
caa agt gct ccc ccc ctt gaa tca ccg caa agg ctc ctc agt tca gaa	2260

[illegible]

<211> 748  
 <212> PRT  
 <213> Homo sapiens

<400> 107

Met Lys Thr Ser Pro Arg Arg Pro Leu Ile Leu Lys Arg Arg Arg Leu  
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Pro Leu Pro Val Gln Asn Ala Pro Ser Glu Thr Ser Glu Glu Glu Pro  
 20 25 30

Lys Arg Ser Pro Ala Gln Gln Glu Ser Asn Gln Ala Glu Ala Ser Lys  
 35 40 45

Glu Val Ala Glu Ser Asn Ser Cys Lys Phe Pro Ala Gly Ile Lys Ile  
 50 55 60

Ile Asn His Pro Thr Met Pro Asn Thr Gln Val Val Ala Ile Pro Asn  
 65 70 75 80

Asn Ala Asn Ile His Ser Ile Ile Thr Ala Leu Thr Ala Lys Gly Lys  
 85 90 95

Glu Ser Gly Ser Ser Gly Pro Asn Lys Phe Ile Leu Ile Ser Cys Gly  
 100 105 110

Gly Ala Pro Thr Gln Pro Pro Gly Leu Arg Pro Gln Thr Gln Thr Ser  
 115 120 125

Tyr Asp Ala Lys Arg Thr Glu Val Thr Leu Glu Thr Leu Gly Pro Lys  
 130 135 140

Pro Ala Ala Arg Asp Val Asn Leu Pro Arg Pro Pro Gly Ala Leu Cys  
 145 150 155 160

Glu Gln Lys Arg Glu Thr Cys Ala Asp Gly Glu Ala Ala Gly Cys Thr  
 165 170 175

Ile Asn Asn Ser Leu Ser Asn Ile Gln Trp Leu Arg Lys Met Ser Ser  
 180 185 190

Asp Gly Leu Gly Ser Arg Ser Ile Lys Gln Glu Met Glu Glu Lys Glu  
 195 200 205

Asn Cys His Leu Glu Gln Arg Gln Val Lys Val Glu Glu Pro Ser Arg  
 210 215 220

Pro Ser Ala Ser Trp Gln Asn Ser Val Ser Glu Arg Pro Pro Tyr Ser  
225 230 235 240

Tyr Met Ala Met Ile Gln Phe Ala Ile Asn Ser Thr Glu Arg Lys Arg  
245 250 255

Met Thr Leu Lys Asp Ile Tyr Thr Trp Ile Glu Asp His Phe Pro Tyr  
260 265 270

Phe Lys His Ile Ala Lys Pro Gly Trp Lys Asn Ser Ile Arg His Asn  
275 280 285

Leu Ser Leu His Asp Met Phe Val Arg Glu Thr Ser Ala Asn Gly Lys  
290 295 300

Val Ser Phe Trp Thr Ile His Pro Ser Ala Asn Arg Tyr Leu Thr Leu  
305 310 315 320

Asp Gln Val Phe Lys Gln Gln Lys Arg Pro Asn Pro Glu Leu Arg Arg  
325 330 335

Asn Met Thr Ile Lys Thr Glu Leu Pro Leu Gly Ala Arg Arg Lys Met  
340 345 350

Lys Pro Leu Leu Pro Arg Val Ser Ser Tyr Leu Val Pro Ile Gln Phe  
355 360 365

Pro Val Asn Gln Ser Leu Val Leu Gln Pro Ser Val Lys Val Pro Leu  
370 375 380

Pro Leu Ala Ala Ser Leu Met Ser Ser Glu Leu Ala Arg His Ser Lys  
385 390 395 400

Arg Val Arg Ile Ala Pro Lys Val Leu Leu Ala Glu Glu Gly Ile Ala  
405 410 415

Pro Leu Ser Ser Ala Gly Pro Gly Lys Glu Glu Lys Leu Leu Phe Gly  
420 425 430

Glu Gly Phe Ser Pro Leu Leu Pro Val Gln Thr Ile Lys Glu Glu Glu  
435 440 445

Ile Gln Pro Gly Glu Glu Met Pro His Leu Ala Arg Pro Ile Lys Val  
450 455 460

Glu Ser Pro Pro Leu Glu Glu Trp Pro Ser Pro Ala Pro Ser Phe Lys  
 465 470 475 480

Glu Glu Ser Ser His Ser Trp Glu Asp Ser Ser Gln Ser Pro Thr Pro  
 485 490 495

Arg Pro Lys Lys Ser Tyr Ser Gly Leu Arg Ser Pro Thr Arg Cys Val  
 500 505 510

Ser Glu Met Leu Val Ile Gln His Arg Glu Arg Arg Glu Arg Ser Arg  
 515 520 525

Ser Arg Arg Lys Gln His Leu Leu Pro Pro Cys Val Asp Glu Pro Glu  
 530 535 540

Leu Leu Phe Ser Glu Gly Pro Ser Thr Ser Arg Trp Ala Ala Glu Leu  
 545 550 555 560

Pro Phe Pro Ala Asp Ser Ser Asp Pro Ala Ser Gln Leu Ser Tyr Ser  
 565 570 575

Gln Glu Val Gly Gly Pro Phe Lys Thr Pro Ile Lys Glu Thr Leu Pro  
 580 585 590

Ile Ser Ser Thr Pro Ser Lys Ser Val Leu Pro Arg Thr Pro Glu Ser  
 595 600 605

Trp Arg Leu Thr Pro Pro Ala Lys Val Gly Gly Leu Asp Phe Ser Pro  
 610 615 620

Val Gln Thr Ser Gln Gly Ala Ser Asp Pro Leu Pro Asp Pro Leu Gly  
 625 630 635 640

Leu Met Asp Leu Ser Thr Thr Pro Leu Gln Ser Ala Pro Pro Leu Glu  
 645 650 655

Ser Pro Gln Arg Leu Leu Ser Ser Glu Pro Leu Asp Leu Ile Ser Val  
 660 665 670

Pro Phe Gly Asn Ser Ser Pro Ser Asp Ile Asp Val Pro Lys Pro Gly  
 675 680 685

Ser Pro Glu Pro Gln Val Ser Gly Leu Ala Ala Asn Arg Ser Leu Thr  
 690 695 700

Glu Gly Leu Val Leu Asp Thr Met Asn Asp Ser Leu Ser Lys Ile Leu  
 705 710 715 720

Leu Asp Ile Ser Phe Pro Gly Leu Asp Glu Asp Pro Leu Gly Pro Asp  
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Asn Ile Asn Trp Ser Gln Phe Ile Pro Glu Leu Gln  
 740 745

<210> 108  
 <211> 19  
 <212> DNA  
 <213> Artificial

<220>  
 <223> A target sequence for siRNA.

<400> 108  
 gcagcagaaa cgaccgaat 19

<210> 109  
 <211> 51  
 <212> DNA  
 <213> Artificial

<220>  
 <223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 109  
 tcccgcagca gaaacgaccg aatttcaaga gaattcggtc gtttctgctg c 51

<210> 110  
 <211> 51  
 <212> DNA  
 <213> Artificial

<220>  
 <223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 110  
 aaaagcagca gaaacgaccg aattctcttg aaattcggtc gtttctgctg c 51

<210> 111  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
 <223> An artificially synthesized hairpin siRNA sequence.

<400> 111  
 gcagcagaaa cgaccgaatt tcaagagaat tcggtcgttt ctgctgc 47

<210> 112  
 <211> 2931  
 <212> DNA  
 <213> Homo sapiens

<220>  
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<400> 112
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ccgctgccgg agcagcccga agggagctgc ggatcgcgag gccagtaccg accccgcccg      120

cccgcgcgca ccgccccgc ccgcc atg gcc cgg gac tac gac cac ctc ttc      172
                               Met Ala Arg Asp Tyr Asp His Leu Phe
                               1                               5

aag ctg ctc atc atc ggc gac agc ggt gtg ggc aag agc agt tta ctg      220
Lys Leu Leu Ile Ile Gly Asp Ser Gly Val Gly Lys Ser Ser Leu Leu
10                               15                               20                               25

ttg cgt ttt gca gac aac act ttc tca ggc agc tac atc acc acg atc      268
Leu Arg Phe Ala Asp Asn Thr Phe Ser Gly Ser Tyr Ile Thr Thr Ile
                               30                               35                               40

gga gtg gat ttc aag atc cgg acc gtg gag atc aac ggg gag aag gtg      316
Gly Val Asp Phe Lys Ile Arg Thr Val Glu Ile Asn Gly Glu Lys Val
                               45                               50                               55

aag ctg cag atc tgg gac aca gcg ggg cag gag cgc ttc cgc acc atc      364
Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile
                               60                               65                               70

acc tcc acg tat tat cgg ggg acc cac ggg gtc att gtg gtt tac gac      412
Thr Ser Thr Tyr Tyr Arg Gly Thr His Gly Val Ile Val Val Tyr Asp
75                               80                               85

gtc acc agt gcc gag tcc ttt gtc aac gtc aag cgg tgg ctt cac gaa      460
Val Thr Ser Ala Glu Ser Phe Val Asn Val Lys Arg Trp Leu His Glu
90                               95                               100                               105

atc aac cag aac tgt gat gat gtg tgc cga ata tta gtg ggt aat aag      508
Ile Asn Gln Asn Cys Asp Asp Val Cys Arg Ile Leu Val Gly Asn Lys
                               110                               115                               120

aat gac gac cct gag cgg aag gtg gtg gag acg gaa gat gcc tac aaa      556
Asn Asp Asp Pro Glu Arg Lys Val Val Glu Thr Glu Asp Ala Tyr Lys
                               125                               130                               135

ttc gcc ggg cag atg ggc atc cag ttg ttc gag acc agc gcc aag gag      604
Phe Ala Gly Gln Met Gly Ile Gln Leu Phe Glu Thr Ser Ala Lys Glu
140                               145                               150

aat gtc aac gtg gaa gag atg ttc aac tgc atc acg gag ctg gtc ctc      652
Asn Val Asn Val Glu Glu Met Phe Asn Cys Ile Thr Glu Leu Val Leu
155                               160                               165

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cga gca aag aaa gac aac ctg gca aaa cag cag cag caa caa cag aac	700
Arg Ala Lys Lys Asp Asn Leu Ala Lys Gln Gln Gln Gln Gln Asn	
170 175 180 185	
gat gtg gtg aag ctc acg aag aac agt aaa cga aag aaa cgc tgc tgc	748
Asp Val Val Lys Leu Thr Lys Asn Ser Lys Arg Lys Lys Arg Cys Cys	
190 195 200	
taa tggcaccag tccactgcag agactgcact gcggtccctc cccagccccg	801
aggcccacgg aggttcctcg ggggacagtc tcagtttctgt gccgttattt aaagaattct	861
ctccatgttt ttgtatcggg aggtgccatc ggcacttctc cccccgccct cctcgagtgc	921
caagaagggtg ttggaccagc ccgcccttcc ctactggtgc cccctcctcc ccggccaagg	981
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acactgcagc ctcgggcact gtggggagtg catgcctggg gcctctgggt ggggaccatg	1881
gacaggccct ggtcactgtc ctaacctttg tcaggacaaa ggtagcaaga ggatttcctg	1941
gcgggtggga aggaatggct ggggcggcca gttttgacac gcccagtgcc cctggagaac	2001
aaccagggtc atctgcactt gatgactgct ccccgacccc cagcccggac acctcattcc	2061
cctcccacta cagggatcaa gtgacctggg aagaaccgag tttaacacca ggatgtgttt	2121
ccttagatatt cctttcctag gcgatttcca gggagagccc tgattggaca atcacatcac	2181
agatcacact gcagtttcca tgtagcact gtggatgggt ttttaatcaa taaaaactgg	2241
gggtttcttc tcaccgactc tccacttgcc caaactgcc aaagctgggt attctgggac	2301
aggccttcac tttggagcca cgggatgggg tgggggagcc ccatgggcct gggaaggagg	2361

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gtgctgtgga gggggctgca gggctgacca gcaggcagcc tcactctggtc gggggcgggg 2421
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2931

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<210> 113
<211> 201
<212> PRT
<213> Homo sapiens

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<400> 113

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Met Ala Arg Asp Tyr Asp His Leu Phe Lys Leu Leu Ile Ile Gly Asp
1          5          10          15

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Ser Gly Val Gly Lys Ser Ser Leu Leu Leu Arg Phe Ala Asp Asn Thr
          20          25          30

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Phe Ser Gly Ser Tyr Ile Thr Thr Ile Gly Val Asp Phe Lys Ile Arg
          35          40          45

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Thr Val Glu Ile Asn Gly Glu Lys Val Lys Leu Gln Ile Trp Asp Thr
          50          55          60

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Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Thr Tyr Tyr Arg Gly
65          70          75          80

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Thr His Gly Val Ile Val Val Tyr Asp Val Thr Ser Ala Glu Ser Phe
          85          90          95

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Val Asn Val Lys Arg Trp Leu His Glu Ile Asn Gln Asn Cys Asp Asp
          100          105          110

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Val Cys Arg Ile Leu Val Gly Asn Lys Asn Asp Asp Pro Glu Arg Lys
          115          120          125

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Val Val Glu Thr Glu Asp Ala Tyr Lys Phe Ala Gly Gln Met Gly Ile  
 130 135 140

Gln Leu Phe Glu Thr Ser Ala Lys Glu Asn Val Asn Val Glu Glu Met  
 145 150 155 160

Phe Asn Cys Ile Thr Glu Leu Val Leu Arg Ala Lys Lys Asp Asn Leu  
 165 170 175

Ala Lys Gln Gln Gln Gln Gln Gln Asn Asp Val Val Lys Leu Thr Lys  
 180 185 190

Asn Ser Lys Arg Lys Lys Arg Cys Cys  
 195 200

<210> 114  
 <211> 19  
 <212> DNA  
 <213> Artificial

<220>  
 <223> A target sequence for siRNA.

<400> 114  
 gagatgttca actgcatca 19

<210> 115  
 <211> 51  
 <212> DNA  
 <213> Artificial

<220>  
 <223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 115  
 tcccgatg ttcaactgca tcattcaaga gatgatgcag ttgaacatct c 51

<210> 116  
 <211> 51  
 <212> DNA  
 <213> Artificial

<220>  
 <223> An artificially synthesized oligonucleotide sequence for siRNA.

<400> 116  
 aaaagatg ttcaactgca tcattctcttg aatgatgcag ttgaacatct c 51

<210> 117  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
 <223> An artificially synthesized hairpin siRNA sequence.  
  
 <400> 117  
 gagatgttca actgcatcat tcaagagatg atgcagttga acatctc 47  
  
 <210> 118  
 <211> 22  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> An artificially synthesized primer sequence for RT-PCR.  
  
 <400> 118  
 aaaaagggga tgcctagaac tc 22  
  
 <210> 119  
 <211> 21  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> An artificially synthesized primer sequence for RT-PCR.  
  
 <400> 119  
 ctttcagcac gtcaaggaca t 21  
  
 <210> 120  
 <211> 23  
 <212> DNA  
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 <220>  
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 <400> 120  
 acacctacga aggtacacat gac 23  
  
 <210> 121  
  
 <211> 23  
 <212> DNA  
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 <400> 121  
 gctatttcag ggtaaattgga gtc 23  
  
 <210> 122  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <223> An artificially synthesized primer sequence for RT-PCR.  
  
 <400> 122  
 cagagatgga ggatgtcaat aac 23  
  
 <210> 123  
 <211> 23  
 <212> DNA  
 <213> Artificial  
  
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 <400> 123  
 catagcagct ttaaagagac acg 23  
  
 <210> 124  
 <211> 21  
 <212> DNA  
 <213> Artificial  
  
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 <223> An artificially synthesized primer sequence for RT-PCR.  
  
 <400> 124  
 ccaccataac agtggagtgg g 21  
  
 <210> 125  
 <211> 24  
 <212> DNA  
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 <223> An artificially synthesized primer sequence for RT-PCR.  
  
 <400> 125  
 cagttacagg tgtatgactg ggag 24  
  
 <210> 126  
 <211> 23  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> An artificially synthesized primer sequence for RT-PCR.  
  
 <400> 126  
 ctgaatacaa cttcctgttt gcc 23  
  
 <210> 127  
 <211> 23  
 <212> DNA  
 <213> Artificial  
  
 <220>

<223> An artificially synthesized primer sequence for RT-PCR.

<400> 127

gaccacagaa ttaccaaaac tgc

23